

# SEQUENCE LISTING

<110> Duvick, Jon

<120> Compositions and Methods for Fummonisin Detoxification

<130> 5718-111

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 1691

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase with intron

<400> 1

```

atgtcggcca ccagcaactc cagaggcgat tgttcogtcg catgcgacgc catcatcggt 60
ggagccggcc tcagcggcat ctctgctgtg tacaaattgc gaaagctcag actcaacgcc 120
aaaatcttcg agggagcccc cgattttggc ggcgtctggc actggaaccg ctaccctggc 180
gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
tggacctggt cttgccgcta tcctgaccag aaagagttgc tgtcatatgt tcaccactgt 300
gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
aagtatctca ttctcgctac ggggttgctc cacaggaagc aactccccgc actccccggc 480
ctgcgcgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
gagggccaga gagtgcgct catcgggtgcc gggggccacaa gcatccagat tgttcaggag 600
ttggccaaga aggtgacca ggtaaccatg tttatgcgaa ggccgagcta ttgtctgccc 660
atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggceta ctacccacag 720
ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcggttggc 780
atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
gcctttaatt ttcttgcttg ccagtaccga gaagtcatgg ttgacaaaaa ggccaaccga 900
ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
gatctcatgg ctctcttgga gccgccgtac tggttcggta ccaagcgtc cccactggag 1020
agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
ccatttgttg ctgttacaaa gacaggtgtg ctcttgagtg acggcagcaa gagggaatgc 1140
gacacgatcg tgctggcgac gggtttcgac agtttctact gctcgtgagt gtgctcgatc 1200
atggctccga gtccggacgt ttggctgacc ttgaaagatt gacacatatg ggcttgaaaa 1260
acaagcacgg agtggacctg aaggaggtgt ggaaagatgg catatctact tatatgggag 1320
tcttctctca tggcttcccc aatgccttct tcgtcgccac ggctcaagcc ccgaccgtcc 1380
tttccaacgg cccaacgatc atagaaaccc aagtcgactt gatcgccgat acaattgcaa 1440

```

```

agttggaggc cgagcacgcc acgtccgttg aggcgacgaa atcagcacia gaggcattggt 1500
cgattatgat tgccaagatg aacgagcaca ctctgttccc cttgacggat tcgtggtgga 1560
ctggaggcaa catccctggg aaagcaacac gtgctttaac cttcataggc gggattgctc 1620
tctatgagca gatctgtcaa gagaagggtg ccaattggga tgggtttgat gtgcttcatg 1680
ctccctgcta a 1691

```

<210> 2

<211> 1638

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, fully spliced cDNA

<400> 2

```

atgtcggcca ccagcaactc cagaggcgat tgttccgtcg catgcgacgc catcatcggt 60
ggagccggcc tcagcggcat ctctgctgtg tacaaattgc gaaagctcag actcaacgcc 120
aaaatcttcg agggagcccc cgatttttggc ggcgtctggc actggaaccg ctaccctggc 180
gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
tggaacctgg cttgccgcta tcctgaccag aaagagttgc tgtcatatgt tcaccactgt 300
gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
aagtatctca ttctcgtac ggggttgctc cacaggaagc aactcccgcc actccccggc 480
ctcgccgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
gagggccaga gagtcgccgt catcgggtgcc ggggccacaa gcatccagat tgttcaggag 600
ttggccaaga aggctgacca ggtaaccatg tttatgcgaa ggccgagcta ttgtctgccc 660
atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctacccacg 720
ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcgggttggc 780
atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
gcctttaatt ttcttgcttg ccagtaccga gaagtcattg ttgacaaaaa ggccaaccga 900
ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
gatctcatgg ctctcttgga gccgcctgac tggttcggta ccaagcgtc cccactggag 1020
agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
cccattgttg ctgttacaaa gacaggtgtg ctcttgagt acggcagcaa gaggggaatgc 1140
gacacgatcg tgctggcgac ggggttcgac agtttcaact gctcattgac acatatgggc 1200
ttgaaaaaca agcacggagt ggacctgaag gaggtgtgga aagatggcat atctacttat 1260
atgggagtct tctctcatgg cttccccaat gccttcttcg tcgccacggc tcaagccccg 1320
accgtccttt ccaacggccc aacgatcata gaaaccaag tcgacttgat cgccgataca 1380
attgcaaagt tggaggccga gcacgccacg tccgttgagg cgacgaaatc agcacaagag 1440
gcatggtcga ttatgattgc caagatgaac gagcacaactc tgttcccctt gaeggattcg 1500
tgggtggactg gaggcaacat ccctgggaaa gcaacacgtg ctttaacctt cataggcggg 1560
attgctctct atgagcagat ctgtcaagag aaggtggcca attgggatgg gtttgatgtg 1620
cttcatgctc cctgctaa 1638

```

<210> 3

<211> 545

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, translation of fully spliced  
cDNA

<400> 3

Met Ser Ala Thr Ser Asn Ser Arg Gly Asp Cys Ser Val Ala Cys Asp  
1 5 10 15

Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys  
20 25 30

Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp  
35 40 45

Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp  
50 55 60

Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp  
65 70 75 80

Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr  
85 90 95

Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe  
100 105 110

Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp  
115 120 125

Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile  
130 135 140

Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly  
145 150 155 160

Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu  
165 170 175

Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala  
180 185 190

Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val  
195 200 205

Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg  
210 215 220

Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr  
 225 230 235 240

Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala  
 245 250 255

Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr  
 260 265 270

Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln  
 275 280 285

Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp  
 290 295 300

Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg  
 305 310 315 320

Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg  
 325 330 335

Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val  
 340 345 350

Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr  
 355 360 365

Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val  
 370 375 380

Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly  
 385 390 395 400

Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly  
 405 410 415

Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe  
 420 425 430

Phe Val Ala Thr Ala Gln Ala Pro Thr Val Leu Ser Asn Gly Pro Thr  
 435 440 445

Ile Ile Glu Thr Gln Val Asp Leu Ile Ala Asp Thr Ile Ala Lys Leu  
 450 455 460

Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu  
 465 470 475 480

Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro  
 485 490 495

Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr  
 500 505 510

Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys  
 515 520 525

Gln Glu Lys Val Ala Asn Trp Asp Gly Phe Asp Val Leu His Ala Pro  
 530 535 540

Cys  
 545

<210> 4

<211> 1464

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> aldehyde dehydrogenase , fully spliced cDNA

<400> 4

```

atggttcttt cgcctgacga atacaagagt gaactcttca tcaacaatga attcgtctcc 60
tccaaggggt ccgagagatt aacgctcacg aaccggtggg acgaatccac cgttgccact 120
gatgttcacg tggccaacgc ggccgatgtc gacagtgcag tagccgcttc ggtgcaggcg 180
gtcaaaaagg gcccatggaa gaagttcaca ggtgcacaac gcgcggcggtg catgcttaag 240
ttcgcggacc tcgccgagaa gaacgccgag aagctcgctc gtctggagtc gctgccacc 300
ggtagaccgg tgtogatgat cactcatttc gacattccaa acatgggtctc cgtgtttcgc 360
tactatgcag gctgggccga caagatcgcc ggaaagacct ttcccagga caacggcaag 420
ccgaattggc gttacgagcc gatgggggtg tgtgctggta ttgccagctg gaacgcgact 480
tttctttacg tcggctggaa gatagcccc gccctcgccg ccggctgctc cttcatcttc 540
aaagcctcgg agaaatcccc gctgggcgtt ctgggcctcg ctctctctt cgcagaagcc 600
ggattccctc ctggagtcgt gcagttcctc actggagcac gagtgcaggg tgaagcattg 660
gcgtcgacac tggacattgc gaagatcagc ttcacaagat ctgtcggcgg tggccgcgcc 720
gtcaagcaag caacactcaa gtccaacatg aagcgcgtca ctctagaact gggggaaaag 780
ccaaccatcg tcttcaacga agctcctctc gaacggcagt cgggggaatc ggcaaaggat 840
ttctcaaaat tcgggcaaat ttgggtcccc ccctcctgtt tgctagtgcg atggggaaat 900
ttagcggaga aattccatgg agtccgtcat ggctcatttg gaggtgtgca gagatggctt 960
ggccagaacc cattggaacc caagaggacg catgggtccct tcgtcgacaa gtcccagtac 1020
gacagagtct tgggtaacat tgacgttggc aaggataccg cgcagctcct cactggcggt 1080
ggtagaaaagg gcgacaaggg attcgcgatt gaaccgacga tatttgtcaa tcccaaacca 1140
ggcagcaaaa tttggtttga ggagatcttt ggccccgtct tgtccattaa gacgttcaag 1200
acggaagaag aggccattga gattgccaat gacacgactt atgggctagc ctcggtcatt 1260
tataccaaat ctctcaacag ggggtctccg gtctcgtcgg cgctcgagac cgggtggcgtc 1320
tcgatcaact tcccctttat ccccagaca caaactccgt ttggcggcat gaaacaatcg 1380

```

ggctcaggca gagagctagg cgaagaaggg ctcaaggcgt acttggagcc caagaccatt 1440  
aatatccacg tcaacataga gtga 1464

<210> 5

<211> 487

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> aldehyde dehydrogenase, translation of fully  
spliced cDNA

<400> 5

Met Val Leu Ser Pro Asp Glu Tyr Lys Ser Glu Leu Phe Ile Asn Asn  
1 5 10 15

Glu Phe Val Ser Ser Lys Gly Ser Glu Arg Leu Thr Leu Thr Asn Pro  
20 25 30

Trp Asp Glu Ser Thr Val Ala Thr Asp Val His Val Ala Asn Ala Ala  
35 40 45

Asp Val Asp Ser Ala Val Ala Ala Ser Val Gln Ala Val Lys Lys Gly  
50 55 60

Pro Trp Lys Lys Phe Thr Gly Ala Gln Arg Ala Ala Cys Met Leu Lys  
65 70 75 80

Phe Ala Asp Leu Ala Glu Lys Asn Ala Glu Lys Leu Ala Arg Leu Glu  
85 90 95

Ser Leu Pro Thr Gly Arg Pro Val Ser Met Ile Thr His Phe Asp Ile  
100 105 110

Pro Asn Met Val Ser Val Phe Arg Tyr Tyr Ala Gly Trp Ala Asp Lys  
115 120 125

Ile Ala Gly Lys Thr Phe Pro Glu Asp Asn Gly Lys Pro Asn Trp Arg  
130 135 140

Tyr Glu Pro Met Gly Val Cys Ala Gly Ile Ala Ser Trp Asn Ala Thr  
145 150 155 160

Phe Leu Tyr Val Gly Trp Lys Ile Ala Pro Ala Leu Ala Ala Gly Cys  
165 170 175

Ser Phe Ile Phe Lys Ala Ser Glu Lys Ser Pro Leu Gly Val Leu Gly  
180 185 190

Leu Ala Pro Leu Phe Ala Glu Ala Gly Phe Pro Pro Gly Val Val Gln  
 195 200 205

Phe Leu Thr Gly Ala Arg Val Thr Gly Glu Ala Leu Ala Ser His Met  
 210 215 220

Asp Ile Ala Lys Ile Ser Phe Thr Arg Ser Val Gly Gly Gly Arg Ala  
 225 230 235 240

Val Lys Gln Ala Thr Leu Lys Ser Asn Met Lys Arg Val Thr Leu Glu  
 245 250 255

Leu Gly Glu Lys Pro Thr Ile Val Phe Asn Glu Ala Pro Leu Glu Arg  
 260 265 270

Gln Ser Gly Glu Ser Ala Lys Asp Phe Ser Lys Phe Gly Gln Ile Trp  
 275 280 285

Val Pro Pro Ser Cys Leu Leu Val Gln Trp Gly Asn Leu Ala Glu Lys  
 290 295 300

Phe His Gly Val Arg His Gly Ser Phe Gly Gly Cys Gln Arg Trp Leu  
 305 310 315 320

Gly Gln Asn Pro Leu Glu Pro Lys Arg Thr His Gly Pro Phe Val Asp  
 325 330 335

Lys Ser Gln Tyr Asp Arg Val Leu Gly Asn Ile Asp Val Gly Lys Asp  
 340 345 350

Thr Ala Gln Leu Leu Thr Gly Val Gly Arg Lys Gly Asp Lys Gly Phe  
 355 360 365

Ala Ile Glu Pro Thr Ile Phe Val Asn Pro Lys Pro Gly Ser Lys Ile  
 370 375 380

Trp Phe Glu Glu Ile Phe Gly Pro Val Leu Ser Ile Lys Thr Phe Lys  
 385 390 395 400

Thr Glu Glu Glu Ala Ile Glu Ile Ala Asn Asp Thr Thr Tyr Gly Leu  
 405 410 415

Ala Ser Val Ile Tyr Thr Lys Ser Leu Asn Arg Gly Leu Arg Val Ser  
 420 425 430

Ser Ala Leu Glu Thr Gly Gly Val Ser Ile Asn Phe Pro Phe Ile Pro  
 435 440 445

Glu Thr Gln Thr Pro Phe Gly Gly Met Lys Gln Ser Gly Ser Gly Arg  
 450 455 460

Glu Leu Gly Glu Glu Gly Leu Lys Ala Tyr Leu Glu Pro Lys Thr Ile  
 465 470 475 480

Asn Ile His Val Asn Ile Glu  
 485

<210> 6

<211> 1764

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> permease, partially spliced cDNA

<400> 6

```
aactatggac tccagaccaa gtggatacgg cttgaaaggc gggacaaggc agacaacgaa 60
gaacacagag acggcggcgg caggtggtgc gtccgagtc ctgaacgttc ctctggagaa 120
gaaacaattt ggcaccatca ccacgtgtgc cttggccttt gtgatttgca acagttgggc 180
tggtatctca ggcagtctcc agctcgccct actagcgggg gggcccgta ctctccttta 240
cggcatacta atcagtactc tcgtctacat ctgcacgct ttctcattag ccgaactgac 300
cagcgtctac ccgactgccg gtggccaata tcattttgcg tcgactcctgg caccaaaatc 360
aatcaatcgg agcatttcat acgtgtgagg actcgtgtcg ttgctttcat ggatcgctat 420
cggaagctca gtgaccatga tacctgctca acagatcccg gcgctgatag ccgcctatag 480
tcacacatac tcccaggatt cgtggcatgt cttcctcatc tacgagggag tcgctgtggt 540
ggtgctcttg ttcaacttgt ttgccctgaa aagaaaccct tgggttcatt aaatcggatt 600
cggcctcagc atcgtctctc tcgtgatctc ctttatcgcc attctagcgc ggtccaaccc 660
caaggctcca aactcacagg tatggactgc ttggagcaac tatactggct ggtccgacgg 720
cgtctgcttc atcctgggcc ttctgacatc ctgcttcatt ttcatggct tggacgcagc 780
aatgcatctg gctgaagaat gcacagatgc tgctcgtacg gtacccaaag cagtggtcag 840
tgcaatcata attggcttct gcaccgcctt tccatataca atcgcagttc tgtatggaat 900
tacagatctc gactctatct taagtccgc cggctatatt ccattcgaga caatgaggca 960
gtctgctcga attcggcttt ttgcaacggg cctctcatgt ggcggtatcg tgatggcctt 1020
cttcgccctc aacgctgtac aagagactgc gtctcgactc acctggagct ttgcccgga 1080
caatgggctg gtattttcca ctcatctcga acgcattcat ccccgctggc aagttcctgt 1140
ttggtctcta ttccgcacct ggggaattct ggccacatgc ggatgtatat ttctagggtc 1200
tagcacagct ttcaatgcct tgggtcaattc cgccgttgta ctccagcaac tctccttctc 1260
gatcccaatc gccctactcc tctacaaaaa gcgagatcca aagttcttgc cgagcactcg 1320
tgcttttgtg ttaccgcgtg gaatcgggtt tctggtcaat gtgctagcgg tggctctcac 1380
gtccgtcacc actgtgtttt tcagcttccc actgaccgtg cctacggccg cgtcaaccat 1440
gaattacaca agtgcgatta taggcgttgc acttgctctt ggtgtcttga actgggtcgt 1500
gcatgccagg aagcattatc agggacccca cttggagctt gacggacggg tcgtcggagc 1560
agaatttcaa gttgggcat gaattggacg aaatggagac gcgtgtgcaa tgtcaaaaat 1620
tgctggggtg gtactgagag tctggattag ctgcaacgcg ggacaaccga gggtagaaca 1680
```



ctctgcaatc gagcaggaca atatcaatta ggcaachasv caaaaaaaaaa aaaaaaaaaa 1740  
 aaaaaagcgg ccgctgaatt ctag 1764

<210> 7

<211> 1578

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> permease, fully spliced cDNA

<400> 7

atggactcca gaccaagtgg atacggcttg aaaggcggga caaggcagac aacgaagaac 60  
 acagagacgg cggcggcagg tgggtgcgtcc gagtccttga acgttcctct ggagaagaaa 120  
 caatttggca ccatcaccat cgtgtccttg gcctttgtga tttgcaacag ttgggctggt 180  
 atctcaggca gtctccagct cgccctacta gcgggggggc ccgtcactct cctttacggc 240  
 atcctaata gtactctcgt ctacatctgc atcgctttct cattagccga actgaccagc 300  
 gtctaccoga ctgccggtgg ccaatatcat tttgcgtcga tcctggcacc aaaatcaatc 360  
 aatcggagca ttccatacgt gtgcggactc gtgtcgttgc tttcatggat cgctatcgga 420  
 agctcagtga ccatgatacc tgcacaacag atcccggcgc tgatagccgc ctatagtcac 480  
 acatactccc aggattcgtg gcatgtcttc ctcatctacg agggagtcgc gctggtggtg 540  
 ctcttgttca acttgtttgc cctgaaaaga aacccttggg ttcatagaaat cggattcggc 600  
 ctacagatcg ctctctctgt gatctccttt atcgccattc tagcgcggtc caaccccaag 660  
 gtcctaaact cacaggtatg gactgcttgg agcaactata ctggctggtc cgacggcgtc 720  
 tgcttcatcc tgggcctttc gacatcctgc ttcattgtca ttggcttggga cgcagcaatg 780  
 catctggctg aagaatgcac agatgctgct cgtacggtac ccaaagcagt ggtcagtgca 840  
 atcataattg gcttctgcac cgcccttcca tatacaatcg cagttctgta tggaattaca 900  
 gatctcgact ctattctaag ttccgcccgc tatattccat tcgagacaat gaggcagtct 960  
 gctcgaattc ggctttttgc aacggctctc tcatgtggcg gtatcgtgat ggccttcttc 1020  
 gccctcaacg ctgtacaaga gactgcttct cgactcacct ggagctttgc ccgggacaat 1080  
 gggctggtat tttccactca tctcgaacgc attcatcccc gctggcaagt tctgttttgg 1140  
 tctctattcg cgacctgggg aattctggcc acatgcggat gtatatttct aggttctagc 1200  
 acagctttca atgccttggc caattccgcc gttgtactcc agcaactctc cttcctgac 1260  
 ccaatcgccc tactcctcta ccaaaagcga gatccaaagt tcttgccgag cactcgtgct 1320  
 tttgtgttac cgcgtggaat cgggtttctg gtcaatgtgc tagcgggtggc cttcacgtcc 1380  
 gtcaccactg tggtttttcag cttccactg accgtgccta cggccgcgtc aacctgaat 1440  
 tacacaagtg cgattatagg cgttgcaact gctcttgggt tcttgaactg ggtcgtgcat 1500  
 gccaggaagc attatcaggg accccacttg gagcttgacg gacgggtcgt cggagcagaa 1560  
 tttcaagttg ggccatga 1578

<210> 8

<211> 525

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> permease, translation of fully spliced cDNA

<400> 8

Met Asp Ser Arg Pro Ser Gly Tyr Gly Leu Lys Gly Gly Thr Arg Gln  
1 5 10 15

Thr Thr Lys Asn Thr Glu Thr Ala Ala Ala Gly Gly Ala Ser Glu Ser  
20 25 30

Leu Asn Val Pro Leu Glu Lys Lys Gln Phe Gly Thr Ile Thr Ile Val  
35 40 45

Ser Leu Ala Phe Val Ile Cys Asn Ser Trp Ala Gly Ile Ser Gly Ser  
50 55 60

Leu Gln Leu Ala Leu Leu Ala Gly Gly Pro Val Thr Leu Leu Tyr Gly  
65 70 75 80

Ile Leu Ile Ser Thr Leu Val Tyr Ile Cys Ile Ala Phe Ser Leu Ala  
85 90 95

Glu Leu Thr Ser Val Tyr Pro Thr Ala Gly Gly Gln Tyr His Phe Ala  
100 105 110

Ser Ile Leu Ala Pro Lys Ser Ile Asn Arg Ser Ile Ser Tyr Val Cys  
115 120 125

Gly Leu Val Ser Leu Leu Ser Trp Ile Ala Ile Gly Ser Ser Val Thr  
130 135 140

Met Ile Pro Ala Gln Gln Ile Pro Ala Leu Ile Ala Ala Tyr Ser His  
145 150 155 160

Thr Tyr Ser Gln Asp Ser Trp His Val Phe Leu Ile Tyr Glu Gly Val  
165 170 175

Ala Leu Val Val Leu Leu Phe Asn Leu Phe Ala Leu Lys Arg Asn Pro  
180 185 190

Trp Val His Glu Ile Gly Phe Gly Leu Thr Ile Ala Leu Phe Val Ile  
195 200 205

Ser Phe Ile Ala Ile Leu Ala Arg Ser Asn Pro Lys Ala Pro Asn Ser  
210 215 220

Gln Val Trp Thr Ala Trp Ser Asn Tyr Thr Gly Trp Ser Asp Gly Val  
225 230 235 240

Cys Phe Ile Leu Gly Leu Ser Thr Ser Cys Phe Met Phe Ile Gly Leu  
245 250 255

Asp Ala Ala Met His Leu Ala Glu Glu Cys Thr Asp Ala Ala Arg Thr  
260 265 270

Val Pro Lys Ala Val Val Ser Ala Ile Ile Ile Gly Phe Cys Thr Ala  
275 280 285

Phe Pro Tyr Thr Ile Ala Val Leu Tyr Gly Ile Thr Asp Leu Asp Ser  
290 295 300

Ile Leu Ser Ser Ala Gly Tyr Ile Pro Phe Glu Thr Met Arg Gln Ser  
305 310 315 320

Ala Arg Ile Arg Leu Phe Ala Thr Val Leu Ser Cys Gly Gly Ile Val  
325 330 335

Met Ala Phe Phe Ala Leu Asn Ala Val Gln Glu Thr Ala Ser Arg Leu  
340 345 350

Thr Trp Ser Phe Ala Arg Asp Asn Gly Leu Val Phe Ser Thr His Leu  
355 360 365

Glu Arg Ile His Pro Arg Trp Gln Val Pro Val Trp Ser Leu Phe Ala  
370 375 380

Thr Trp Gly Ile Leu Ala Thr Cys Gly Cys Ile Phe Leu Gly Ser Ser  
385 390 395 400

Thr Ala Phe Asn Ala Leu Val Asn Ser Ala Val Val Leu Gln Gln Leu  
405 410 415

Ser Phe Leu Ile Pro Ile Ala Leu Leu Leu Tyr Gln Lys Arg Asp Pro  
420 425 430

Lys Phe Leu Pro Ser Thr Arg Ala Phe Val Leu Pro Arg Gly Ile Gly  
435 440 445

Phe Leu Val Asn Val Leu Ala Val Val Phe Thr Ser Val Thr Thr Val  
450 455 460

Phe Phe Ser Phe Pro Leu Thr Val Pro Thr Ala Ala Ser Thr Met Asn  
465 470 475 480

Tyr Thr Ser Ala Ile Ile Gly Val Ala Leu Ala Leu Gly Val Leu Asn  
485 490 495

Trp Val Val His Ala Arg Lys His Tyr Gln Gly Pro His Leu Glu Leu  
500 505 510

Asp Gly Arg Val Val Gly Ala Glu Phe Gln Val Gly Pro  
515 520 525

<210> 9

<211> 3999

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, with introns

<400> 9

tatttsccat ctmckatgaa tggcagatga atcggagaaa cctcgaccaa accaagatgg 60  
cagtgaagtcg tcctcacacc ctcccccaga aaaggaaacc gaaggcagta tttcagacta 120  
tctacgaatc ttcagatatg ccgacaaata cgactggact ctcaatgtca tcgcgctcat 180  
ctgcgccatc ggatccggggg cttcccttcc tctgatgtcg atcatcttcg gtagcttcac 240  
caacaagttc aacaattaca attcggggcg cgggagtcct gaagcgttca aggccgatgt 300  
ggatcatttc gtctgtgtgt tcgtctacct ctttattggg aagtttgtcc tcacgtacgt 360  
ttccacggct gccattacca tttcagctat acgaaccact cgaactcttc gacgagtgtt 420  
ccttgaatgc accttgccggc aagaggtctg gcatttcgac aagcagagca atggagcaat 480  
cgccactcag gtcactacca atggcaaccg tatacaaaca ggtattgccg agaaattggg 540  
ctttaccgtg caggcacttt caatgttctt ttctgcattt gtggtcgctt tggcgtctca 600  
gtggaagcta gctttaatca ccatgtccgt catccctgcc attttcctgg tcaccggcat 660  
ctgcatagca attgatgccg ctcaggaggc caggatcacc aggatctact cacgcgccgc 720  
tgtcctcgca gaagaagtct tatcatccat ccggacagtc catgctttct acgcccagaa 780  
gaaaatggtc gaaaaatatg atgtcttttt gcagcaagca caccaagaag ggaagaagaa 840  
atcgccaaat tatgggtctt tgtttctaac tgagtacttt tgcatttacg ctgctatcgc 900  
actgggcctt ttgggaaagg tttttcgcat gtatcagaat ggcgagggtg ccgacgttgg 960  
caaagtcttt actggtgcct ttccgtcacc tttagcagcc acgtccatct caatgcttgc 1020  
gccttcaggt tcagtcgttt accaacgcgc catcttcggc ctccgaatta ttcagtatca 1080  
ttgacaaacc cacgcagctc gacccttctc gacccttttt ggaaagcagc cagagggctg 1140  
cttaggtcaa attgatgcc aaaacctggc atttgcctac ccctcccgcac catctgcca 1200  
agtacttcca gatttcaact tgacaattcc agctggcaag acgacggccc tcgtcgggtgc 1260  
atcaggtagc ggcaaaagca caatggctcg cttacttgaa cggtggtatc tgcccagttc 1320  
ggggaggata ttacttgatg gggttgaact gggacaatac aatgtgaaat ggctgagaag 1380  
ccgcattcgc ctcggtcaac aggaacctgt gttgtttcgt ggcacaatct tccagaacat 1440  
tgccaacggt ttcattgatg agcaacgaga tctgcctcgc gaaaaacaaa tggagcttgt 1500  
gcaaaaagct tgcaaagcag caatgccgac gtgttcatta atgagcttcc gaacggttat 1560  
gagactgaag ttggcgagcg agccggagcc ttgagtggag gtcaacaagc cgaattgcaa 1620  
tcgcacgaag tatcatatcg gatcccaaga tcctgttact cgatgaagct accagcgccc 1680  
ttgacccgaa ggcggagaaa gtggtccagg aggccttgaa ccgagtgtcc aaagaccgca 1740  
ctactttggt cattgcccac aaactagcca ctgtcatagc actcactatt agggcgatt 1800  
gggccctcta gatgcatgct cgagcggccg ccagtgtgac gaattgatgc agaattcggc 1860  
ttgtcattac gccgcactgg tgcgtgcaca ggacctcggg gctgacgaac aagaagaaca 1920  
tgagaagacc ctgcacgaaa aggcagcacg agaagctgct ggtgaacgac cggcacttga 1980  
gcgcactcac accactgcca catctcaagc tggagacctg gagaagcgga aggtgcgggt 2040

cgggactttg ggctactcgc tcctaaaatg catcctaate atgttctacg aacaaaaaaaa 2100  
 tctctactgg tgcttcttgt tgtcaacaat agcgggttctg atatgcgcgg ccacatttcc 2160  
 aggacaagcc cttttgtttt cgagattgct cactgtcttc gagttgagtg gtcattgcggc 2220  
 acaggaacgg gcagactttt atagtctgat gttctttgtc gtggctctag gaaatctagt 2280  
 aggatatttc acgattggct ggacatgcaa cgttggttca caagttgtca cccatcgcta 2340  
 tcgagccgaa atgttccaac gactactgga tcaagacatc gaattcttcg acatcccgga 2400  
 gaatacttct ggtgctctca catcgcaact gtcagctcta cccacgcagt tgcaggagtt 2460  
 gatatcaaca aattcttctc atttttatcg ttgtcgtaca acatcctctc gagcagtgct 2520  
 ctgacactag cctatggatg gaaactgggc ctgggtggtg tggttggtgc acttccaccc 2580  
 ctgcttttgg ctggctacct cagaattcgt cttgagacga agctagaagc cggaaactcg 2640  
 gcaaaacttt cagaaagtgc tgggcttgca agcgaagcag ttaccgcgat cgggaccgtc 2700  
 tcatctttga ctctcgaagg scatgttctc caacagtaact cggacatggt gagcaaggtc 2760  
 gtgctaagat catccaaagc tttggtttgg acgatgtttt ggttctcact gtcacagtcg 2820  
 atcgagtttc tggctatggc cctgggaatt ttggtatggg aagtcgacta ctggcttcag 2880  
 gtgaggtacg acacaactca attttatatc atcttcgtgg gcgttttgtt tgccgggtcca 2940  
 agcagcagcc cagaagccga attactccac gactcttacc aaggctcggg cggctgcgaa 3000  
 ctatatcttc tggctgcgga cattgaagcc gaccatccgc gaaacggagg agaacaagaa 3060  
 aaaagggcca gtgggtggat gccctgtcga cctcgaggac attgaattca ggtatcgtca 3120  
 acgtgattcg gctcgagttc tccgcggggg ttccatgaca atcgagccag gacaatttgt 3180  
 agcttatgtg ggcgcttctg gctgtggcaa gtcaacgttg atcgctttgt tggaacgatt 3240  
 ctacgaccgc acctcgggcc gaatttccatt tgcacacgag aatattgcag aaatgtcgcc 3300  
 gcgcttgtag cgcggccata tgtctttggt ccaacaggaa cccacayttt accaaggctc 3360  
 cgttcgcgag aatgtgacgt tggccctcga agccgaatta tcagaagagc tttgtcaagg 3420  
 acgccttccc gcaaggccaa tgctttggat tttgtcatct ctttaccaga aggctttgaa 3480  
 acgccttgcg gctcaacgag ggatgcagtt ctccggcggg caacgacagc ggatcgccat 3540  
 cgcaagagca ttgattcgaa atccaaagct gttgctactt gacgaagcga cgtcagccct 3600  
 cgacacgcaa tcggaacgct tggttcaagc tgccctcgat gaggcattcca cgagccgaac 3660  
 gacaatagca gtggcgacc gactttccac tattcggaat gttgatgtta tttttgtgtt 3720  
 tgccaacggg agaatcgccg aaacgggcac tcacgcgga ctacaacgac tgagaggaag 3780  
 atattacgag atgtgtttg cacaatcttt agaccaagca tgagcgttca cagagaagcg 3840  
 gaaaagggcg gtgggatctt ttaggatagg tttagtggcg tgttacttac tacaggcggt 3900  
 tggattcagg tacgacaact tgtacaataa gtagcataga gcatgtaatg aaagggtact 3960  
 cgtcccggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3999

<210> 10

<211> 3792

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, fully spliced cDNA

<400> 10

atggcagatg aatcggagaa acctcgacca aaccaagatg gcagtgagtc gtccctcacac 60  
 cctccccag aaaaggaaac cgaaggcagt atttcagact atctacgaat cttcagatat 120  
 gccgacaaat acgactggac tctcaatgtc atcgcgctca tctgcgcat cggatccggg 180  
 gcttcccttc ctctgatgtc gatcatcttc ggtagcttca ccaacaagtt caacaattac 240  
 aattcggggc acggggagtc tgaagcgctc aaggccgatg tggatcattt cgtcctgtgg 300

ttcgtctacc	tctttattgg	gaagtttgtc	ctcacgtacg	tttccacggc	tgccattacc	360
atttcagcta	tacgaaccac	tcgaactcct	cgacgagtgt	tccttgaatg	caccttgcg	420
caagaggtct	ggcatttcga	caagcagagc	aatggagcaa	tcgccactca	rgtcactacc	480
aatggcaacc	gtatacaaac	aggtattgcc	gagaaattgg	tctttaccgt	gcaggcactt	540
tcaatgttct	tttctgcatt	tgtggtcgct	ttggcgctct	agtggaagct	agctttaatc	600
accatgtccg	tcacccctgc	cattttcctg	gtcacccgca	tctgcatagc	aattgatgcc	660
gctcaggagg	ccaggatcac	caggatctac	tcacgcgcgc	ctgtcctcgc	agaagaagtc	720
ttatcatcca	tccggacagt	ccatgctttc	tacgcccaga	agaaaatggt	cgaaaaatat	780
gatgtctttt	tgacgaagc	acaccaagaa	gggaagaaga	aatcgccaaa	taatggsctc	840
ttgttctcaa	ctgagtactt	ttgcatttac	gctgctatcg	cactggcctt	ttggaaaggt	900
tttcgcatgt	atcagaatgg	cgaggttgcc	gacgttgcca	aagtctttac	tgttgctcct	960
tccgtcacct	tagcagccac	gtccatctca	atgcttgccg	cttcagggtt	agtcggtttac	1020
caacgccgca	tcttcggctc	cgaattattc	agtatcattg	acaaaccac	gcagctcgac	1080
cctctcgacc	cttctggaaa	gcagccagag	ggctgcctag	gtcaaattga	gatccaaaac	1140
ctggcatttg	cctaccctc	ccgaccatct	gcccaggtac	ttcgagattt	caacttgaca	1200
attccagctg	gcaagacgac	ggccctcgct	ggtgcatcag	gtagcggcaa	aagcacaatg	1260
gtcggcttac	ttgaacgggt	gtatctgccc	agttcgggga	ggatattact	tgatgggttg	1320
gaactgggac	aatacaatgt	gaaatggctg	agaagccgca	ttcgccctcg	tcaacaggaa	1380
cctgtgttgt	ttcgtggcac	aatcttccag	aacattgcca	acggtttcat	ggatgagcaa	1440
cgagatctgc	ctcgcgaaaa	acaaatggag	cttgtgcaaa	aagcttgcaa	agccagcaat	1500
ggcgacgtgt	tcattaatga	gcttccgaac	ggttatgaga	ctgaagttgg	cgagcgagcc	1560
ggagccttga	gtggagggtca	acgacaacga	attgcaatcg	cacgaagtat	catatcggat	1620
cccaagatcc	tgttactcga	tgaagctacc	agcgcccttg	acccgaaggc	ggagaaagtg	1680
gtccaggagg	ccttgaaccg	agtgtccaaa	gaccgcacta	ctttgggtcat	tgcccacaaa	1740
ctagccactg	tcaaaagtgc	tggcaacatc	gcagtcattt	cccaggggaa	aatcgtcgag	1800
caaggcacac	accacgaatt	gatcgaattc	ggctgtcatt	acgccgcact	ggtgcgtgca	1860
caggacctcg	gggctgacga	acaacaagaa	catgagaaga	ccctgcacga	aaaggcagca	1920
cgagaagctg	ctggtgaacg	accggcactt	gagcgcactc	acaccactgc	cacatctcaa	1980
gctggagacc	tggagaagcg	gaagggtgcc	gtcgggactt	tgggctactc	gctcctaaaa	2040
tgcacccctaa	tcatgttcta	cgaacaaaaa	aatctctact	ggtgcttctt	gttgtcaaca	2100
ataacggttc	tgatatgcgc	ggccacattt	ccaggacaag	cccttttggt	ttcgagattg	2160
ctcactgtct	tcgagttgag	tggatcatgc	gcacaggaa	gggcagactt	ttatattctg	2220
atgttctttg	tcgtggctct	aggaaatcta	gtaggatatt	tcacgattgg	ctggacatgc	2280
aacgttatct	cacaagttgt	cacccatcgc	tatcaagccg	caatgttcca	acgagtactg	2340
gatcaagaca	tcgaactcct	cgacatcccg	gagcaaattt	ctggtgctct	cacatcgcaa	2400
ctgtcagctc	taccacgca	gttgcaagag	ttgatatcag	caaattttct	catttatatc	2460
gttgctcggtc	aacatcgctc	cgagcagtg	tctaccacta	gcctatggat	ggaaactggg	2520
cctgggtggt	gtgtttggtg	cacttccacc	cctgcttttg	gctggctacc	tcagaattcg	2580
tctagagacg	aagctagaag	ccggaaactc	ggcaaacttt	gcagaaagtg	ctgggcttgc	2640
aagcgaagca	gttaccgcga	tccggaccgt	ctcatctttg	actctcgaag	gccatgttct	2700
ccaacagtac	tcggacatgt	tgagcaaggt	cttgctaaga	tcacccaaag	cttttggttt	2760
ggacgatgtt	ttggttttca	cttgtcacag	tcgatggagt	ttttggctat	tgccctggga	2820
ttttgtattg	cagtcgataa	ttggcttcag	gtgagtacga	cacaactcaa	ttttatatca	2880
tcttcgtggg	cgttttggtt	gccggtocaa	gcagcagccc	agtatttggt	ttactccacg	2940
agttttacca	aggctcggtc	ggctgcgaac	tatatcctct	ggctgcggac	attgaagccg	3000
accatccgcg	aaacggagga	gaacaagaaa	aaaggcccag	tgggtggatg	ccctgtcgac	3060
ctcgaggaca	ttgaattcag	gtatcgtcaa	cgtgattcgg	ctcgagttct	ccgcgggggt	3120
tccatgacaa	tcgagccagg	acaatttgta	gcttatgtgg	gcgcttctgg	ctgtggcaag	3180

tcaacgttga tcgctttgtc ggaacgattc tacgaccgga cctcggggccg aatttcattt 3240  
gcacacgaga atattgcaga aatgtcgccg cgcttgtacc gcggccatat gtctttggtc 3300  
caacaggaac ccacacttta ccaaggctcc gttcgcgaga atgtgacgtt ggccctcgaa 3360  
gccgaattat cagaagagct ttgtcaagga cgccttcccg caaggccaat gctttggatt 3420  
ttgtcatctc tttaccagaa ggctttgaaa cgccttgccg ctcaacgagg gatgcagttc 3480  
tccggcgggc aacgacagcg gatcgccatc gcaagagcat tgattcgaaa tccaaagctg 3540  
ttgctacttg acgaagcgac gtcagccctc gacacgcaat cggaacgtct ggttcaagct 3600  
gccctcgatg aggcattccac gagccgaacg acaatagcag tggcgccaccg actttccact 3660  
attcggaatg ttgatgttat ttttgtgttt gccaaaggga gaatcgccga aacgggcact 3720  
cacgcggaac tacaacgact gagaggaaga tattacgaga tgtgtttggc acaatcttta 3780  
gaccaagcat ga 3792

<210> 11

<211> 1263

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> p-glycoprotein, translation of fully spliced cDNA

<400> 11

Met Ala Asp Glu Ser Glu Lys Pro Arg Pro Asn Gln Asp Gly Ser Glu  
1 5 10 15

Ser Ser Ser His Pro Pro Pro Glu Lys Glu Thr Glu Gly Ser Ile Ser  
20 25 30

Asp Tyr Leu Arg Ile Phe Arg Tyr Ala Asp Lys Tyr Asp Trp Thr Leu  
35 40 45

Asn Val Ile Ala Leu Ile Cys Ala Ile Gly Ser Gly Ala Ser Leu Pro  
50 55 60

Leu Met Ser Ile Ile Phe Gly Ser Phe Thr Asn Lys Phe Asn Asn Tyr  
65 70 75 80

Asn Ser Gly Asp Gly Ser Pro Glu Ala Phe Lys Ala Asp Val Asp His  
85 90 95

Phe Val Leu Trp Phe Val Tyr Leu Phe Ile Gly Lys Phe Val Leu Thr  
100 105 110

Tyr Val Ser Thr Ala Ala Ile Thr Ile Ser Ala Ile Arg Thr Thr Arg  
115 120 125

Thr Leu Arg Arg Val Phe Leu Glu Cys Thr Leu Arg Gln Glu Val Trp  
130 135 140

His Phe Asp Lys Gln Ser Asn Gly Ala Ile Ala Thr Xaa Val Thr Thr  
 145 150 155 160

Asn Gly Asn Arg Ile Gln Thr Gly Ile Ala Glu Lys Leu Val Phe Thr  
 165 170 175

Val Gln Ala Leu Ser Met Phe Phe Ser Ala Phe Val Val Ala Leu Ala  
 180 185 190

Ser Gln Trp Lys Leu Ala Leu Ile Thr Met Ser Val Ile Pro Ala Ile  
 195 200 205

Phe Leu Val Thr Gly Ile Cys Ile Ala Ile Asp Ala Ala Gln Glu Ala  
 210 215 220

Arg Ile Thr Arg Ile Tyr Ser Arg Ala Ala Val Leu Ala Glu Glu Val  
 225 230 235 240

Leu Ser Ser Ile Arg Thr Val His Ala Phe Tyr Ala Gln Lys Lys Met  
 245 250 255

Val Glu Lys Tyr Asp Val Phe Leu Gln Gln Ala His Gln Glu Gly Lys  
 260 265 270

Lys Lys Ser Pro Asn Asn Gly Val Leu Phe Ser Thr Glu Tyr Phe Cys  
 275 280 285

Ile Tyr Ala Ala Ile Ala Leu Ala Phe Trp Lys Gly Phe Arg Met Tyr  
 290 295 300

Gln Asn Gly Glu Val Ala Asp Val Gly Lys Val Phe Thr Val Val Leu  
 305 310 315 320

Ser Val Thr Leu Ala Ala Thr Ser Ile Ser Met Leu Ala Pro Ser Gly  
 325 330 335

Ser Val Val Tyr Gln Arg Arg Ile Phe Gly Ser Glu Leu Phe Ser Ile  
 340 345 350

Ile Asp Lys Pro Thr Gln Leu Asp Pro Leu Asp Pro Ser Gly Lys Gln  
 355 360 365

Pro Glu Gly Cys Leu Gly Gln Ile Glu Ile Gln Asn Leu Ala Phe Ala  
 370 375 380

Tyr Pro Ser Arg Pro Ser Ala Gln Val Leu Arg Asp Phe Asn Leu Thr  
 385 390 395 400



Ile Pro Ala Gly Lys Thr Thr Ala Leu Val Gly Ala Ser Gly Ser Gly  
405 410 415

Lys Ser Thr Met Val Gly Leu Leu Glu Arg Trp Tyr Leu Pro Ser Ser  
420 425 430

Gly Arg Ile Leu Leu Asp Gly Leu Glu Leu Gly Gln Tyr Asn Val Lys  
435 440 445

Trp Leu Arg Ser Arg Ile Arg Leu Val Gln Gln Glu Pro Val Leu Phe  
450 455 460

Arg Gly Thr Ile Phe Gln Asn Ile Ala Asn Gly Phe Met Asp Glu Gln  
465 470 475 480

Arg Asp Leu Pro Arg Glu Lys Gln Met Glu Leu Val Gln Lys Ala Cys  
485 490 495

Lys Ala Ser Asn Gly Asp Val Phe Ile Asn Glu Leu Pro Asn Gly Tyr  
500 505 510

Glu Thr Glu Val Gly Glu Arg Ala Gly Ala Leu Ser Gly Gly Gln Arg  
515 520 525

Gln Arg Ile Ala Ile Ala Arg Ser Ile Ile Ser Asp Pro Lys Ile Leu  
530 535 540

Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Pro Lys Ala Glu Lys Val  
545 550 555 560

Val Gln Glu Ala Leu Asn Arg Val Ser Lys Asp Arg Thr Thr Leu Val  
565 570 575

Ile Ala His Lys Leu Ala Thr Val Lys Ser Ala Gly Asn Ile Ala Val  
580 585 590

Ile Ser Gln Gly Lys Ile Val Glu Gln Gly Thr His His Glu Leu Ile  
595 600 605

Glu Phe Gly Cys His Tyr Ala Ala Leu Val Arg Ala Gln Asp Leu Gly  
610 615 620

Ala Asp Glu Gln Gln Glu His Glu Lys Thr Leu His Glu Lys Ala Ala  
625 630 635 640

Arg Glu Ala Ala Gly Glu Arg Pro Ala Leu Glu Arg Thr His Thr Thr  
645 650 655

Ala Thr Ser Gln Ala Gly Asp Leu Glu Lys Arg Lys Val Pro Val Gly  
660 665 670

Thr Leu Gly Tyr Ser Leu Leu Lys Cys Ile Leu Ile Met Phe Tyr Glu  
675 680 685

Gln Lys Asn Leu Tyr Trp Cys Phe Leu Leu Ser Thr Ile Thr Val Leu  
690 695 700

Ile Cys Ala Ala Thr Phe Pro Gly Gln Ala Leu Leu Phe Ser Arg Leu  
705 710 715 720

Leu Thr Val Phe Glu Leu Ser Gly His Ala Ala Gln Glu Arg Ala Asp  
725 730 735

Phe Tyr Ile Leu Met Phe Phe Val Val Ala Leu Gly Asn Leu Val Gly  
740 745 750

Tyr Phe Thr Ile Gly Trp Thr Cys Asn Val Ile Ser Gln Val Val Thr  
755 760 765

His Arg Tyr Gln Ala Ala Met Phe Gln Arg Val Leu Asp Gln Asp Ile  
770 775 780

Glu Leu Leu Asp Ile Pro Glu Gln Ile Ser Gly Ala Leu Thr Ser Gln  
785 790 795 800

Leu Ser Ala Leu Pro Thr Gln Leu Gln Glu Leu Ile Ser Ala Asn Phe  
805 810 815

Leu Ile Tyr Ile Val Val Gly Gln His Arg Leu Glu Gln Cys Ser Thr  
820 825 830

Thr Ser Leu Trp Met Glu Thr Gly Pro Gly Gly Cys Val Trp Cys Thr  
835 840 845

Ser Thr Pro Ala Phe Gly Trp Leu Pro Gln Asn Ser Ser Arg Asp Glu  
850 855 860

Ala Arg Ser Arg Lys Leu Gly Lys Leu Cys Arg Lys Cys Trp Ala Cys  
865 870 875 880

Lys Arg Ser Ser Tyr Arg Asp Pro Asp Arg Leu Ile Phe Asp Ser Arg  
885 890 895

Arg Pro Cys Ser Pro Thr Val Leu Gly His Val Glu Gln Gly Leu Ala  
900 905 910

Lys Ile Ile Gln Ser Phe Trp Phe Gly Arg Cys Phe Gly Phe His Leu  
 915 920 925

Ser Gln Ser Met Glu Phe Leu Ala Ile Ala Leu Gly Phe Cys Ile Ala  
 930 935 940

Val Asp Asn Trp Leu Gln Val Ser Thr Thr Gln Leu Asn Phe Ile Ser  
 945 950 955 960

Ser Ser Trp Ala Phe Cys Leu Pro Val Gln Ala Ala Ala Gln Tyr Leu  
 965 970 975

Ala Tyr Ser Thr Ser Phe Thr Lys Ala Arg Ser Ala Ala Asn Tyr Ile  
 980 985 990

Leu Trp Leu Arg Thr Leu Lys Pro Thr Ile Arg Glu Thr Glu Glu Asn  
 995 1000 1005

Lys Lys Lys Gly Pro Val Gly Gly Cys Pro Val Asp Leu Glu Asp Ile  
 1010 1015 1020

Glu Phe Arg Tyr Arg Gln Arg Asp Ser Ala Arg Val Leu Arg Gly Val  
 1025 1030 1035 1040

Ser Met Thr Ile Glu Pro Gly Gln Phe Val Ala Tyr Val Gly Ala Ser  
 1045 1050 1055

Gly Cys Gly Lys Ser Thr Leu Ile Ala Leu Ser Glu Arg Phe Tyr Asp  
 1060 1065 1070

Pro Thr Ser Gly Arg Ile Ser Phe Ala His Glu Asn Ile Ala Glu Met  
 1075 1080 1085

Ser Pro Arg Leu Tyr Arg Gly His Met Ser Leu Val Gln Gln Glu Pro  
 1090 1095 1100

Thr Leu Tyr Gln Gly Ser Val Arg Glu Asn Val Thr Leu Ala Leu Glu  
 1105 1110 1115 1120

Ala Glu Leu Ser Glu Glu Leu Cys Gln Gly Arg Leu Pro Ala Arg Pro  
 1125 1130 1135

Met Leu Trp Ile Leu Ser Ser Leu Tyr Gln Lys Ala Leu Lys Arg Leu  
 1140 1145 1150

Ala Ala Gln Arg Gly Met Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile  
 1155 1160 1165

Ala Ile Ala Arg Ala Leu Ile Arg Asn Pro Lys Leu Leu Leu Leu Asp  
1170 1175 1180

Glu Ala Thr Ser Ala Leu Asp Thr Gln Ser Glu Arg Leu Val Gln Ala  
1185 1190 1195 1200

Ala Leu Asp Glu Ala Ser Thr Ser Arg Thr Thr Ile Ala Val Ala His  
1205 1210 1215

Arg Leu Ser Thr Ile Arg Asn Val Asp Val Ile Phe Val Phe Ala Asn  
1220 1225 1230

Gly Arg Ile Ala Glu Thr Gly Thr His Ala Glu Leu Gln Arg Leu Arg  
1235 1240 1245

Gly Arg Tyr Tyr Glu Met Cys Leu Ala Gln Ser Leu Asp Gln Ala  
1250 1255 1260

1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500